Amendments to the Specification:

In the BRIEF DESCRIPTION OF THE DRAWINGS section, please replace the paragraph beginning at page 7, line 7 with the following amended paragraph:

Figure 1A(1-8)-B: Primary sequence of mSlo3

Figure 1A(1-8): Alignment of primary sequence of mSlo3 with BK Ca^{2+}-activated K^+ channels mSlo1 (mouse) and dSlo1 (*Drosophila*). Hydrophobic segments are designated S0 through S10. Segments S1-S6 represent the transmembrane segments that surround pore of the channel. The region designated "Calcium Bowl" has been implicated in the regulation of mSlo1 by calcium. The core and tail domain structure of Slo1 has been conserved (Wei *et al., Neuron* 13:671-681 (1994)). mSlo3 residues 35 through 641 encompass S0 through S8, the core domain, and share 56% and 50% identity with mSlo1 and dSlo1 while interspecies homologs mSlo1 and dSlo1 exhibit 62% identity in this region. mSlo3 residues 686-1136 encompassing S9 and S10, the tail, share 39% identity with mSlo1 and dSlo1 while the interspecies homologs mSlo1 and dSlo1 share 68% identity in this region. A region having no significant homology between mSlo1 and mSlo3 is found between S8 and S9. An arrowhead indicates a phenylalanine residue (F) in a region critical for ion selectivity.

Please replace the paragraph beginning on page 10, line 23 with the following paragraph:

Structurally, the full length nucleotide sequence of mSlo3 (SEQ ID NO:2) encodes a protein of 1113 amino acids (SEQ ID NO:1) with a predicted molecular mass of 126 kDa. hSlo3 encodes a protein of a similar size and expression pattern (see Example II). Slo3 is a member of the Slo of potassium channel protein family as evidenced by sequence homology to the BK calcium-activated potassium channel (Slo1; *see* Figure 1A(1-8)). The hydrophilicity profiles of Slo1 and Slo3 sequences indicate 11 hydrophobic segments, S0 through S10, which can be divided into "core" and "tail" domains (Figure 1B). Within the core domain (hydrophobic regions S0-S8 of Slo3 proteins) mSlo3 and the sequenced region of hSlo3 share at least 61.5% amino acid identity, while mSlo1 and mSlo3 share 51% identity in this region.

Homology in the core domain is much higher than in the tail domain, which is involved in calcium sensing (Wei *et al., Neuron* 13:671-681 (1994)).

Please replace the paragraph beginning on page 56, line 2 with the following paragraph:

mSlo3 cDNA was isolated from a testis cDNA library based on its homology to the large-conductance calcium-activated (BK) potassium channel, mSlo1 (Butler *et al., Science* 261:221-224 (1993)). The probe was generated from an expressed sequence tag identified in the GenBank database. The new channel was termed mSlo3 ("m" denoting derivation from mouse). Figure 1A(1-8) illustrates that the 1113 amino acid mSlo3 is similar to the 1196 amino acid mSlo1 protein (Butler *et al.*, 1993, *supra*) as well as *Drosophila* Slo1 (Atkinson *et al., Science* 253:551-553 (1991); Adelman *et al.*, 1992, *supra*). The hydrophilicity profiles of both sequences indicate 11 hydrophobic segments, S0 through S10 (Figure 1B). As with mSlo1, these can be divided into "core" and "tail" domains. Homology of mSlo3 to mSlo1 in the core domain (S0-S8) (51%), which is generally conserved in the voltage-gated superfamily of K^+ channels, is much higher than in the tail domain, which is involved in calcium sensing (Wei *et al., Neuron* 13:671-681 (1994)).

Amendments to the Drawings:

Attached hereto are fourteen (14) sheets of formal drawings as requested by the Examiner in the Notice of Allowance.

It is requested that the attached formal drawings be substituted for the drawings originally filed herein.

The drawing changes do not involve new matter and address the objections raised in the Notice of Draftsperson's Patent Drawing Review.

Attachment: Replacement Sheets (14 sheets of formal drawings)